

SEQUENCE LISTING

<110> KATO, Seishi
NAGATA, Naoki
FUJIMURA, Naoko
KOBAYASHI, Midori
ITO, Koichi
ISHIZUKA, Yoshiko

<120> A Method for Producing an Antibody by Gene Immunization

<130> 2002-0400A/LC/00653

<140> 10/088,859

<141> 2002-05-29

<150> PCT/JP01/06371

<151> 2001-07-24

<150> JP2000-222743

<151> 2000-07-24

<150> JP2000-254407

<151> 2000-08-24

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 697

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (151)..(600)

<400> 1

```
tatacctcta gtttggagct gtgctgtaaa aacaagagta acatttttat attaaagtta 60
aataaagtta caactttgaa gagagtttct gcaagacatg acacaaagct gctagcagaa 120
aatcaaaacg ctgattaaaa gaagcacggt atg atg acc aaa cat aaa aag tgt 174
                               Met Met Thr Lys His Lys Lys Cys
                               1                               5

ttt ata att gtt ggt gtt tta ata aca act aat att att act ctg ata 222
Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile
    10                               15                               20

gtt aaa cta act cga gat tct cag agt tta tgc ccc tat gat tgg att 270
Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile
    25                               30                               35                               40

ggg ttc caa aac aaa tgc tat tat ttc tct aaa gaa gaa gga gat tgg 318
Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp
```

45 50 55
 aat tca agt aaa tac aac tgt tcc act caa cat gcc gac cta act ata 366
 Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile
 60 65 70
 att gac aac ata gaa gaa atg aat ttt ctt agg cgg tat aaa tgc agt 414
 Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser
 75 80 85
 tct gat cac tgg att gga ctg aag atg gca aaa aat cga aca gga caa 462
 Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln
 90 95 100
 tgg gta gat gga gct aca ttt acc aaa tcg ttt ggc atg aga ggg agt 510
 Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser
 105 110 115 120
 gaa gga tgt gcc tac ctc agc gat gat ggt gca gca aca gct aga tgt 558
 Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys
 125 130 135
 tac acc gaa aga aaa tgg att tgc agg aaa aga ata cac taa 600
 Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His
 140 145
 gttaatgtct aagataatgg ggaaaataga aaataacatt attaagtgtgta aaaccagcaa 660
 agtacttttt taattaaaca aagttcgagt tttgtac 697

<210> 2
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Met Thr Lys His Lys Lys Cys Phe Ile Ile Val Gly Val Leu Ile
 1 5 10 15
 Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln
 20 25 30
 Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr
 35 40 45
 Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
 50 55 60
 Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn
 65 70 75 80
 Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys
 85 90 95
 Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr
 100 105 110
 Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp
 115 120 125
 Asp Gly Ala Ala Thr Ala Arg Cys Tyr Thr Glu Arg Lys Trp Ile Cys
 130 135 140
 Arg Lys Arg Ile His
 145

gcctgaatgc ctttg

548

<210> 4
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu Ala Thr Gly Glu Lys
 1 5 10 15
 Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
 20 25 30
 Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
 35 40 45
 Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
 50 55 60
 Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp
 65 70 75 80
 Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
 85 90 95
 Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
 100 105 110
 Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
 115 120 125
 Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
 130 135 140
 Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
 145 150 155

<210> 5
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence: Synthesized oligonucleotide

<400> 5
 cccgatatct catggcgacg cccctaagc 30

<210> 6
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence: Synthesized oligonucleotide

<400> 6
 cccgatatct caatggtgag gcttctctgg 30

<210> 7
 <211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Sequence: Synthesized oligonucleotide

<400> 7

cccgaattca tggcgacgcc ccctaagc

28

<210> 8

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial Sequence: Synthesized oligonucleotide

<400> 8

cccgtcgacg catggtgagg cttctctggg aa

32

<210> 9

<211> 1643

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (25)..(915)

<400> 9

aacatctggg	gacagcggga	aaac	atg	agt	gac	tcc	aag	gaa	cca	agg	gtg	51
			Met	Ser	Asp	Ser	Lys	Glu	Pro	Arg	Val	
			1				5					

cag	cag	ctg	ggc	ctc	ctg	ggg	tgt	ctt	ggc	cat	ggc	gcc	ctg	gtg	ctg	99
Gln	Gln	Leu	Gly	Leu	Leu	Gly	Cys	Leu	Gly	His	Gly	Ala	Leu	Val	Leu	
10				15					20					25		

caa	ctc	ctc	tcc	ttc	atg	ctc	ttg	gct	ggg	gtc	ctg	gtg	gcc	atc	ctt	147
Gln	Leu	Leu	Ser	Phe	Met	Leu	Leu	Ala	Gly	Val	Leu	Val	Ala	Ile	Leu	
			30					35						40		

gtc	caa	gtg	tcc	aag	gtc	ccc	agc	tcc	cta	agt	cag	gaa	caa	tcc	gag	195
Val	Gln	Val	Ser	Lys	Val	Pro	Ser	Ser	Leu	Ser	Gln	Glu	Gln	Ser	Glu	
			45				50						55			

caa	gac	gca	atc	tac	cag	aac	ctg	acc	cag	ctt	aaa	gct	gca	gtg	ggc	243
Gln	Asp	Ala	Ile	Tyr	Gln	Asn	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly	
		60				65						70				

gag	ctc	tca	gag	aaa	tcc	aag	ctg	cag	gag	atc	tac	cag	gag	ctg	acc	291
Glu	Leu	Ser	Glu	Lys	Ser	Lys	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	
		75				80					85					

cag	ctg	aag	gct	gca	gtg	ggc	gag	ttg	cca	gag	aaa	tcc	aag	ctg	cag	339
Gln	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln	

90.	95	100	105	
gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg				387
Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu	110	115	120	
cca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc cgg ctg				435
Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu	125	130	135	
aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc				483
Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile	140	145	150	
tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg cca gag				531
Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu	155	160	165	
aaa tcc aag ctg cag gag atc tac cag gag ctg acg gag ctg aag gct				579
Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala	170	175	180	185
gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc tac cag				627
Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln	190	195	200	
gag ctg acc cag ctg aag gct gca gtg ggt gag ttg cca gac cag tcc				675
Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser	205	210	215	
aag cag cag caa atc tat caa gaa ctg acc gat ttg aag act gca ttt				723
Lys Gln Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe	220	225	230	
gaa cgc ctg tgc cgc cac tgt ccc aag gac tgg aca ttc ttc caa gga				771
Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly	235	240	245	
aac tgt tac ttc atg tct aac tcc cag cgg aac tgg cac gac tcc gtc				819
Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Val	250	255	260	265
acc gcc tgc cag gaa gtg agg gcc cag ctc gtc gta atc aaa act gct				867
Thr Ala Cys Gln Glu Val Arg Ala Gln Leu Val Val Ile Lys Thr Ala	270	275	280	
gag gag cag ctt cca gcg gta ctg gaa cag tgg aga acc caa caa tag				915
Glu Glu Gln Leu Pro Ala Val Leu Glu Gln Trp Arg Thr Gln Gln	285	290	295	
cggaatgaa gactgtgcgg aatttagtgg cagtggctgg aacgacaatc gatgtgacgt				975
tgacaattac tggatctgca aaaagcccg agcctgcttc agagacgaat agttgtttcc				1035
ctgctagcct cagcctccat tgtggtatag cagaacttca cccacttgta agccagcgct				1095
tcttctctcc atccttgac cttcacaat gccctgagac gggtctctgt tcgatttttc				1155

atccccatg aacctgggtc ttattctgtc cttctgatgc ctccaagttt cctggtgta 1215
gagcttgtgt tcttggcca tccttgagc ttataagtg acctgagtgg gatgcattta 1275
gggggcgggc ttggtatgtt gtatgaatcc actctctgtt ccttttgag attagactat 1335
ttggattcat gtgtagctgc cctgtccctt ggggctttat ctcatccatg caaactacca 1395
tctgctcaac ttccagctac accccgtgca cccttttgac tggggacttg ctggttgaag 1455
gagctcatct tgcaggctgg aagcaccagg gaattaattc cccagtcaa ccaatggcat 1515
ccagagaggg catggaggct ccatacaacc tcttcacccc ccacatcttt cttgtccta 1575
tacatgtctt ccatttggtt gtttctgagt tgtagccttt ataataaagt ggtaaatgtt 1635
gtaactgc 1643

<210> 10
<211> 2186
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (118)..(1236)

<400> 10
actctttctt cggctcgcga gctgagagga gcaggtagag gggcagaggc gggactgtcg 60
tctgggggag ccgcccagga ggctcctcag gccgacccca gacctgggtt ggccagg 117
atg aag tat ctc cgg cac cgg cgg ccc aat gcc acc ctc att ctg gcc 165
Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
1 5 10 15
atc ggc gct ttc acc ctc ctc ctc ttc agt ctg cta gtg tca cca ccc 213
Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
20 25 30
acc tgc aag gtc cag gag cag cca ccg gcg atc ccc gag gcc ctg gcc 261
Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
35 40 45
tgg ccc act cca ccc acc cgc cca gcc ccg gcc ccg tgc cat gcc aac 309
Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn
50 55 60
acc tct atg gtc acc cac ccg gac ttc gcc acg cag ccg cag cac gtt 357
Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val
65 70 75 80
cag aac ttc ctc ctg tac aga cac tgc cgc cac ttt ccc ctg ctg cag 405
Gln Asn Phe Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln
85 90 95

gac gtg ccc ccc tct aag tgc gcg cag ccg gtc ttc ctg ctg ctg gtg	453
Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val	
100 105 110	
atc aag tcc tcc cct agc aac tat gtg cgc cgc gag ctg ctg cgg cgc	501
Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg	
115 120 125	
acg tgg ggc cgc gag cgc aag gta cgg ggt ttg cag ctg cgc ctc ctc	549
Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu Gln Leu Arg Leu Leu	
130 135 140	
ttc ctg gtg ggc aca gcc tcc aac ccg cac gag gcc cgc aag gtc aac	597
Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu Ala Arg Lys Val Asn	
145 150 155 160	
cgg ctg ctg gag ctg gag gca cag act cac gga gac atc ctg cag tgg	645
Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly Asp Ile Leu Gln Trp	
165 170 175	
gac ttc cac gac tcc ttc ttc aac ctc acg ctc aag cag gtc ctg ttc	693
Asp Phe His Asp Ser Phe Phe Asn Leu Thr Leu Lys Gln Val Leu Phe	
180 185 190	
tta cag tgg cag gag aca agg tgc gcc aac gcc agc ttc gtg ctc aac	741
Leu Gln Trp Gln Glu Thr Arg Cys Ala Asn Ala Ser Phe Val Leu Asn	
195 200 205	
ggg gat gat gac gtc ttt gca cac aca gac aac atg gtc ttc tac ctg	789
Gly Asp Asp Asp Val Phe Ala His Thr Asp Asn Met Val Phe Tyr Leu	
210 215 220	
cag gac cat gac cct ggc cgc cac ctc ttc gtg ggg caa ctg atc caa	837
Gln Asp His Asp Pro Gly Arg His Leu Phe Val Gly Gln Leu Ile Gln	
225 230 235 240	
aac gtg ggc ccc atc cgg gct ttt tgg agc aag tac tat gtg cca gag	885
Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr Val Pro Glu	
245 250 255	
gtg gtg act cag aat gag cgg tac cca ccc tat tgt ggg ggt ggt ggc	933
Val Val Thr Gln Asn Glu Arg Tyr Pro Pro Tyr Cys Gly Gly Gly Gly	
260 265 270	
ttc ttg ctg tcc cgc ttc acg gcc gct gcc ctg cgc cgt gct gcc cat	981
Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu Arg Arg Ala Ala His	
275 280 285	
gtc ttg gac atc ttc ccc att gat gat gtc ttc ctg ggt atg tgt ctg	1029
Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe Leu Gly Met Cys Leu	
290 295 300	
gag ctt gag gga ctg aag cct gcc tcc cac agc ggc atc cgc acg tct	1077
Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile Arg Thr Ser	
305 310 315 320	


```

ggc gtg cgg gct cca tcg caa cac ctg tcc tcc ttt gac ccc tgc ttc 1125
Gly Val Arg Ala Pro Ser Gln His Leu Ser Ser Phe Asp Pro Cys Phe
325 330 335

tac cga gac ctg ctg ctg gtg cac cgc ttc cta cct tat gag atg ctg 1173
Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu
340 345 350

ctc atg tgg gat gcg ctg aac cag ccc aac ctc acc tgc ggc aat cag 1221
Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln
355 360 365

aca cag atc tac tga gtcagcatca ggtccccag cctctgggct cctgtttcca 1276
Thr Gln Ile Tyr
370

taggaagggg cgacaccttc ctcccaggaa gctgagacct ttgtggtctg agcataaggg 1336

agtgccaggg aaggtttgag gtttgatgag tgaatattct ggctggcgaa ctccacaca 1396

tccttcaaaa cccacctggt actgttccag catcttcctt ggatggctgg aggaactcca 1456

gaaaatatcc atcttctttt tgtggtctgt aatggcagaa gtgcctgtgc tagagttcca 1516

actgtggatg catccgtccc gtttgagtca aagtcttact tccctgctct cacctactca 1576

cagacgggat gctaagcagt gcacctgcag tggtttaatg gcagataagc tccgtctgca 1636

gttcagggcc agccagaaac tcctgtgtcc acatagagct gacgtgagaa atatctttca 1696

gcccaggaga gaggggtcct gatcttaacc ctttcctggg tctcagacaa ctcagaaggt 1756

tggggggata ccagagaggt ggtggaatag gaccgcccc tccttacttg tgggatcaaa 1816

tgctgtaatg gtggaggtgt gggcagagga gggaggcaag tgcctttga aagttgtgag 1876

agctcagagt ttctggggtc ctcatagga gccccatcc ctgtgttccc caagaattca 1936

gagaacagca ctggggctgg aatgatcttt aatggggcca aggccaacag gcatatgcct 1996

cactactgcc tggagaaggg agagattcag gtccctccagc agcctccctc acccagtatg 2056

ttttacagat tacgggggga ccgggtgagc cagtgacccc ctgcagcccc cagcttcagg 2116

cctcagtgtc tgccagtcaa gcttcacagg cattgtgatg gggcagcctt ggggaatata 2176

aaattttgtg 2186

```

```

<210> 11
<211> 814
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (145)..(693)

```

<400> 11

agaatcccgg acagccctgc tccctgcagc caggtgtagt ttcgggagcc actggggcca 60

aagtgagagt ccagcgggtct tccagcgctt gggccacggc ggcggccctg ggagcagagg 120

tggagcgacc ccattacgct aaag atg aaa ggc tgg ggt tgg ctg gcc ctg 171
 Met Lys Gly Trp Gly Trp Leu Ala Leu
 1 5

ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat 219
 Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
 10 15 20 25

ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa 267
 Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
 30 35 40

att gcc cag gtg gac ccc aag aag acc att cag atg gga tct ttc cgg 315
 Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
 45 50 55

atc aat cca gat ggc agc cag tca gtg gtg gag gtg cct tat gcc cgc 363
 Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr Ala Arg
 60 65 70

tca gag gcc cac ctc aca gag ctg ctg gag gag ata tgt gac cgg atg 411
 Ser Glu Ala His Leu Thr Glu Leu Leu Glu Glu Ile Cys Asp Arg Met
 75 80 85

aag gag tat ggg gaa cag att gat cct tcc acc cat cgc aag aac tac 459
 Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys Asn Tyr
 90 95 100 105

gta cgt gta gtg ggc cgg aat gga gaa tcc agt gaa ctg gac cta caa 507
 Val Arg Val Val Gly Arg Asn Gly Glu Ser Ser Glu Leu Asp Leu Gln
 110 115 120

ggc atc cga atc gac tca gat att agc ggc acc ctc aag ttt gcg tgt 555
 Gly Ile Arg Ile Asp Ser Asp Ile Ser Gly Thr Leu Lys Phe Ala Cys
 125 130 135

gag agc att gtg gag gaa tac gag gat gaa ctc att gaa ttc ttt tcc 603
 Glu Ser Ile Val Glu Glu Tyr Glu Asp Glu Leu Ile Glu Phe Phe Ser
 140 145 150

cga gag gct gac aat gtt aaa gac aaa ctt tgc agt aag cga aca gat 651
 Arg Glu Ala Asp Asn Val Lys Asp Lys Leu Cys Ser Lys Arg Thr Asp
 155 160 165

ctt tgt gac cat gcc ctg cac ata tcg cat gat gag cta tga 693
 Leu Cys Asp His Ala Leu His Ile Ser His Asp Glu Leu
 170 175 180

accactggag cagccacac tggcttgatg gatcaccccc aggaggggaa aatggtggca 753

atgccttttta tatattatgt ttttactgaa attaactgaa aaaatatgaa accaaaagta 813

c

814

<210> 12
 <211> 695
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (73)..(564)

<400> 12
 aagatttcag ctgcgggacg gtcaggggag acctccaggc gcaggggaagg acggccaggg 60
 tgacacggaa gc atg cga cgg ctg ctg atc cct ctg gcc ctg tgg ctg ggc 111
 Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly
 1 5 10

gcg gtg ggc gtg ggc gtc gcc gag ctc acg gaa gcc cag cgc cgg ggc 159
 Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly
 15 20 25

ctg cag gtg gcc ctg gag gaa ttt cac aag cac ccg ccc gtg cag tgg 207
 Leu Gln Val Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp
 30 35 40 45

gcc ttc cag gag acc agt gtg gag agc gcc gtg gac acg ccc ttc cca 255
 Ala Phe Gln Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro
 50 55 60

gct gga ata ttt gtg agg ctg gaa ttt aag ctg cag cag aca agc tgc 303
 Ala Gly Ile Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys
 65 70 75

cgg aag agg gac tgg aag aaa ccc gag tgc aaa gtc agg ccc aat ggg 351
 Arg Lys Arg Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly
 80 85 90

agg aaa cgg aaa tgc ctg gcc tgc atc aaa ctg gcc tct gag gac aaa 399
 Arg Lys Arg Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys
 95 100 105

gtt ctg ggc cgg ttg gtc cac tgc ccc ata gag acc caa gtt ctg cgg 447
 Val Leu Gly Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg
 110 115 120 125

gag gct gag gag cac cag gag acc cag tgc ctc agg gtg cag cgg gct 495
 Glu Ala Glu Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala
 130 135 140

ggt gag gac ccc cac agc ttc tac ttc cct gga cag ttc gcc ttc tcc 543
 Gly Glu Asp Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser
 145 150 155

aag gcc ctg ccc cgc agc taa gccagcactg agctgcgtgg tgcctccagg 594

Lys Ala Leu Pro Arg Ser
160

accgctgccg gtggtaacca gtggaagacc ccagcccca gggagaggac cccgttctat 654
ccccagccat gataataaag ctgctctccc agctgctct c 695

<210> 13
<211> 1451
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (105)..(1436)

<400> 13
actgcctgga aacgggctgg gcctgcctcg gacgccgccg gtgtcgcgga ttctctttcc 60
gcccgtcca tggcgggtgga tgctgactg gaagcccag tggg atg cgg ctg acg 116
Met Arg Leu Thr
1

cgg aag cgg ctc tgc tgc ttt ctt atc gcc ctg tac tgc cta ttc tcc 164
Arg Lys Arg Leu Cys Ser Phe Leu Ile Ala Leu Tyr Cys Leu Phe Ser
5 10 15 20

ctc tac gct gcc tac cac gtc ttc ttc ggg cgc cgc cgc cag gcg ccg 212
Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg Arg Gln Ala Pro
25 30 35

gcc ggg tcc ccg cgg ggc ctc agg aag ggg gcg gcc ccc gcg cgg gag 260
Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala Pro Ala Arg Glu
40 45 50

aga cgc ggc cga gaa cag tcc act ttg gaa agt gaa gaa tgg aat cct 308
Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu Glu Trp Asn Pro
55 60 65

tgg gaa gga gat gaa aaa aat gag caa caa cac aga ttt aaa act agc 356
Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg Phe Lys Thr Ser
70 75 80

ctt caa ata tta gat aaa tcc acg aaa gga aaa aca gat ctc agt gta 404
Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr Asp Leu Ser Val
85 90 95 100

caa atc tgg ggc aaa gct gcc att ggc ttg tat ctc tgg gag cat att 452
Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu Trp Glu His Ile
105 110 115

ttt gaa ggc tta ctt gat ccc agc gat gtg act gct caa tgg aga gaa 500
Phe Glu Gly Leu Leu Asp Pro Ser Asp Val Thr Ala Gln Trp Arg Glu
120 125 130

gga aag tca atc gta gga aga aca cag tac agc ttc atc act ggt cca 548

Gly	Lys	Ser	Ile	Val	Gly	Arg	Thr	Gln	Tyr	Ser	Phe	Ile	Thr	Gly	Pro		
		135					140					145					
gct	gta	ata	cca	ggg	tac	ttc	tcc	gtt	gat	gtg	aat	aat	gtg	gta	ctc	596	
Ala	Val	Ile	Pro	Gly	Tyr	Phe	Ser	Val	Asp	Val	Asn	Asn	Val	Val	Leu		
	150					155					160						
att	tta	aat	gga	aga	gaa	aaa	gca	aag	atc	ttt	tat	gcc	acc	cag	tgg	644	
Ile	Leu	Asn	Gly	Arg	Glu	Lys	Ala	Lys	Ile	Phe	Tyr	Ala	Thr	Gln	Trp		
165					170					175					180		
tta	ctt	tat	gca	caa	aat	tta	gtg	caa	att	caa	aaa	ctc	cag	cat	ctt	692	
Leu	Leu	Tyr	Ala	Gln	Asn	Leu	Val	Gln	Ile	Gln	Lys	Leu	Gln	His	Leu		
			185						190						195		
gct	gtt	gtt	ttg	ctc	gga	aat	gaa	cat	tgt	gat	aat	gag	tgg	ata	aac	740	
Ala	Val	Val	Leu	Leu	Gly	Asn	Glu	His	Cys	Asp	Asn	Glu	Trp	Ile	Asn		
			200					205					210				
cca	ttc	ctc	aaa	aga	aat	gga	ggc	ttc	gtg	gag	ctg	ctt	ttc	ata	ata	788	
Pro	Phe	Leu	Lys	Arg	Asn	Gly	Gly	Phe	Val	Glu	Leu	Leu	Phe	Ile	Ile		
			215				220						225				
tat	gac	agc	ccc	tgg	att	aat	gac	gtg	gat	gtt	ttt	cag	tgg	cct	tta	836	
Tyr	Asp	Ser	Pro	Trp	Ile	Asn	Asp	Val	Asp	Val	Phe	Gln	Trp	Pro	Leu		
	230					235					240						
gga	gta	gca	aca	tac	agg	aat	ttt	cct	gtg	gtg	gag	gca	agt	tgg	tca	884	
Gly	Val	Ala	Thr	Tyr	Arg	Asn	Phe	Pro	Val	Val	Glu	Ala	Ser	Trp	Ser		
245					250					255					260		
atg	ctg	cat	gat	gag	agg	cca	tat	tta	tgt	aat	ttc	tta	gga	acg	att	932	
Met	Leu	His	Asp	Glu	Arg	Pro	Tyr	Leu	Cys	Asn	Phe	Leu	Gly	Thr	Ile		
				265					270						275		
tat	gaa	aat	tca	tcc	aga	cag	gca	cta	atg	aac	att	ttg	aaa	aaa	gat	980	
Tyr	Glu	Asn	Ser	Ser	Arg	Gln	Ala	Leu	Met	Asn	Ile	Leu	Lys	Lys	Asp		
			280					285					290				
ggg	aac	gat	aag	ctt	tgt	tgg	gtt	tca	gca	aga	gaa	cac	tgg	cag	cct	1028	
Gly	Asn	Asp	Lys	Leu	Cys	Trp	Val	Ser	Ala	Arg	Glu	His	Trp	Gln	Pro		
			295				300						305				
cag	gaa	aca	aat	gaa	agt	ctt	aag	aat	tac	caa	gat	gcc	ttg	ctt	cag	1076	
Gln	Glu	Thr	Asn	Glu	Ser	Leu	Lys	Asn	Tyr	Gln	Asp	Ala	Leu	Leu	Gln		
			310				315					320					
agt	gat	ctc	aca	ttg	tgc	ccg	gtc	gga	gta	aac	aca	gaa	tgc	tat	cga	1124	
Ser	Asp	Leu	Thr	Leu	Cys	Pro	Val	Gly	Val	Asn	Thr	Glu	Cys	Tyr	Arg		
325					330					335					340		
atc	tat	gag	gct	tgc	tcc	tat	ggc	tcc	att	cct	gtg	gtg	gaa	gac	gtg	1172	
Ile	Tyr	Glu	Ala	Cys	Ser	Tyr	Gly	Ser	Ile	Pro	Val	Val	Glu	Asp	Val		
				345					350						355		
atg	aca	gct	ggc	aac	tgt	ggg	aat	aca	tct	gtg	cac	cac	ggt	gct	cct	1220	
Met	Thr	Ala	Gly	Asn	Cys	Gly	Asn	Thr	Ser	Val	His	His	Gly	Ala	Pro		

360	365	370	
ctg cag tta ctc aag tcc atg ggt gct ccc ttt atc ttt atc aag aac			1268
Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile Phe Ile Lys Asn			
375	380	385	
tggt aag gaa ctc cct gct gtt tta gaa aaa gag aaa act ata att tta			1316
Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys Thr Ile Ile Leu			
390	395	400	
caa gaa aaa att gaa aga aga aaa atg tta ctt cag tgg tat cag cac			1364
Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln Trp Tyr Gln His			
405	410	415	420
ttc aag aca gag ctt aaa atg aaa ttt act aat att tta gaa agc tca			1412
Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile Leu Glu Ser Ser			
425	430	435	
ttt tta atg aat aat aaa agt taa ttatcttttt gagct			1451
Phe Leu Met Asn Asn Lys Ser			
440			

*All
Good*
